

Mr. J. Anderson



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,042

DATE: 09/23/2002

TIME: 13:00:09

Input Set : A:\38621224.app

Output Set: N:\CRF3\09232002\I914042.raw

ENTERED

P.6

3 <110> APPLICANT: SCHLESSINGER, JOSEPH  
 4 ANDREEV, JULIAN  
 6 <120> TITLE OF INVENTION: PYK2 BINDING PROTEINS  
 8 <130> FILE REFERENCE: 038602/1224  
 10 <140> CURRENT APPLICATION NUMBER: 09/914,042  
 11 <141> CURRENT FILING DATE: 2001-08-22  
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/04647  
 14 <151> PRIOR FILING DATE: 2000-02-18  
 16 <150> PRIOR APPLICATION NUMBER: 60/121,125  
 17 <151> PRIOR FILING DATE: 1999-02-22  
 19 <160> NUMBER OF SEQ ID NOS: 8  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1006  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Homo sapiens  
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 32 Asp Tyr Lys Ala Pro Thr Ala Ser Ser Phe Thr Thr Arg Thr Ala Gln  
 33 20 25 30  
 35 Cys Arg Asn Thr Val Ala Ala Ile Glu Glu Ala Leu Asp Val Asp Arg  
 36 35 40 45  
 38 Met Val Leu Tyr Lys Met Lys Lys Ser Val Lys Ala Ile Asn Ser Ser  
 39 50 55 60  
 41 Gly Leu Ala His Val Glu Asn Glu Glu Gln Tyr Thr Gln Ala Leu Glu  
 42 65 70 75 80  
 44 Lys Phe Gly Gly Asn Cys Val Cys Arg Asp Asp Pro Asp Leu Gly Ser  
 45 85 90 95  
 47 Ala Phe Leu Lys Phe Ser Val Phe Thr Lys Glu Leu Thr Ala Leu Phe  
 48 100 105 110  
 50 Lys Asn Leu Ile Gln Asn Met Asn Asn Ile Ile Ser Phe Pro Leu Asp  
 51 115 120 125  
 53 Ser Leu Leu Lys Lys Gly Asp Leu Lys Gly Val Lys Gly Asp Leu Lys Lys  
 54 130 135 140  
 56 Pro Phe Asp Lys Ala Trp Lys Asp Tyr Glu Thr Lys Ile Thr Lys Ile  
 57 145 150 155 160  
 59 Glu Lys Glu Lys Lys Glu His Ala Lys Leu His Gly Met Ile Arg Thr  
 60 165 170 175  
 62 Glu Ile Ser Gly Ala Glu Ile Ala Glu Glu Met Glu Lys Glu Arg Arg  
 63 180 185 190  
 65 Phe Phe Gln Leu Gln Met Cys Glu Tyr Leu Leu Lys Val Asn Glu Ile  
 66 195 200 205

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68 Lys Ile Lys Lys Gly Val Asp Leu Leu Gln Asn Leu Ile Lys Tyr Phe
69      210      215      220
71 His Ala Gln Cys Asn Phe Phe Gln Asp Gly Leu Lys Ala Val Glu Ser
72 225      230      235      240
74 Leu Lys Pro Ser Ile Glu Thr Leu Ser Thr Asp Leu His Thr Ile Lys
75      245      250      255
77 Gln Ala Gln Asp Glu Glu Arg Arg Gln Leu Ile Gln Leu Arg Asp Ile
78      260      265      270
80 Leu Lys Ser Ala Leu Gln Val Glu Gln Lys Glu Asp Ser Gln Ile Arg
81      275      280      285
83 Gln Ser Thr Ala Tyr Ser Leu His Gln Pro Gln Gly Asn Lys Glu His
84      290      295      300
86 Gly Thr Glu Arg Asn Gly Ser Leu Tyr Lys Lys Ser Asp Gly Ile Arg
87 305      310      315      320
89 Lys Val Trp Gln Lys Arg Lys Cys Ser Val Lys Asn Gly Phe Leu Thr
90      325      330      335
92 Ile Ser His Gly Thr Ala Asn Arg Pro Pro Ala Lys Leu Asn Leu Leu
93      340      345      350
95 Thr Cys Gln Val Lys Thr Asn Pro Glu Glu Lys Lys Cys Phe Asp Leu
96      355      360      365
98 Ile Ser His Asp Arg Thr Tyr His Phe Gln Ala Glu Asp Glu Gln Glu
99      370      375      380
101 Cys Gln Ile Trp Met Ser Val Leu Gln Asn Ser Lys Glu Glu Ala Leu
102 385      390      395      400
104 Asn Asn Ala Phe Lys Gly Asp Asp Asn Thr Gly Glu Asn Asn Ile Val
105      405      410      415
107 Gln Glu Leu Thr Lys Glu Ile Ile Ser Glu Val Gln Arg Met Thr Gly
108      420      425      430
110 Asn Asp Val Cys Cys Asp Cys Gly Ala Pro Asp Pro Thr Trp Leu Ser
111      435      440      445
113 Thr Asn Leu Gly Ile Leu Thr Cys Ile Glu Cys Ser Gly Ile His Arg
114      450      455      460
116 Glu Leu Gly Val His Tyr Ser Pro Met Gln Ser Leu Thr Leu Asp Val
117 465      470      475      480
119 Leu Gly Thr Ser Glu Leu Leu Leu Ala Lys Asn Ile Gly Asn Ala Gly
120      485      490      495
122 Phe Asn Glu Ile Met Glu Cys Cys Leu Pro Ala Glu Asp Ser Val Lys
123      500      505      510
125 Pro Asn Pro Gly Ser Asp Met Asn Ala Arg Lys Asp Tyr Ile Thr Ala
126      515      520      525
128 Lys Tyr Ile Glu Arg Arg Tyr Ala Arg Lys Lys His Ala Asp Asn Ala
129      530      535      540
131 Ala Lys Leu His Ser Leu Cys Glu Ala Val Lys Thr Arg Asp Ile Phe
132 545      550      555      560
134 Gly Leu Leu Gln Ala Tyr Ala Asp Gly Val Asp Leu Thr Glu Lys Ile
135      565      570      575
137 Pro Leu Ala Asn Gly His Glu Pro Asp Glu Thr Ala Leu His Leu Ala
138      580      585      590
140 Val Arg Ser Val Asp Arg Thr Ser Leu His Ile Val Asp Phe Leu Val

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141          595          600          605
143 Gln Asn Ser Gly Asn Leu Asp Lys Gln Thr Gly Lys Gly Ser Thr Ala
144          610          615          620
146 Leu His Tyr Cys Cys Leu Thr Asp Asn Ala Glu Cys Leu Lys Leu Leu
147 625          630          635          640
149 Leu Arg Gly Lys Ala Ser Ile Glu Ile Ala Asn Glu Ser Gly Glu Thr
150          645          650          655
152 Pro Leu Asp Ile Ala Lys Arg Leu Lys His Glu His Cys Glu Glu Leu
153          660          665          670
155 Leu Thr Gln Ala Leu Ser Gly Arg Phe Asn Ser His Val His Val Glu
156          675          680          685
158 Tyr Glu Trp Arg Leu Leu His Glu Asp Leu Asp Glu Ser Asp Asp Asp
159          690          695          700
161 Met Asp Glu Lys Leu Gln Pro Ser Glu Asn Arg Arg Glu Asp Arg Pro
162 705          710          715          720
164 Ile Ser Phe Tyr Gln Leu Gly Ser Asn Gln Leu Gln Ser Asn Ala Val
165          725          730          735
167 Ser Leu Ala Arg Asp Ala Ala Asn Leu Ala Lys Glu Lys Gln Arg Ala
168          740          745          750
170 Phe Met Pro Ser Ile Leu Gln Asn Glu Thr Tyr Gly Ala Leu Leu Ser
171          755          760          765
173 Gly Ser Pro Pro Pro Ala Gln Pro Ala Ala Pro Ser Thr Thr Ser Ala
174          770          775          780
176 Pro Pro Leu Pro Pro Arg Asn Val Gly Lys Val Gln Thr Ala Ser Ser
177 785          790          795          800
179 Ala Asn Thr Leu Trp Lys Thr Asn Ser Val Ser Val Asp Gly Gly Ser
180          805          810          815
182 Arg Gln Arg Ser Ser Ser Asp Pro Pro Ala Val His Pro Pro Leu Pro
183          820          825          830
185 Pro Leu Arg Val Thr Ser Thr Asn Pro Leu Thr Pro Thr Pro Pro Pro
186          835          840          845
188 Pro Val Ala Lys Thr Pro Ser Val Met Glu Ala Leu Ser Gln Pro Ser
189          850          855          860
191 Lys Pro Ala Pro Pro Gly Ile Ser Gln Ile Arg Pro Pro Pro Leu Pro
192 865          870          875          880
194 Pro Gln Pro Pro Ser Arg Leu Pro Gln Lys Lys Pro Ala Pro Gly Thr
195          885          890          895
197 Asp Lys Ser Thr Pro Leu Thr Asn Lys Gly Gln Pro Arg Gly Pro Val
198          900          905          910
200 Asp Leu Ser Ala Thr Glu Ala Leu Gly Pro Leu Ser Asn Ala Met Val
201          915          920          925
203 Leu Gln Pro Pro Ala Pro Met Pro Arg Lys Ser Gln Ala Thr Lys Leu
204          930          935          940
206 Lys Pro Lys Arg Val Lys Ala Leu Tyr Asn Cys Val Ala Asp Asn Pro
207 945          950          955          960
209 Asp Glu Leu Thr Phe Ser Glu Gly Asp Val Ile Ile Val Asp Gly Glu
210          965          970          975
212 Glu Asp Gln Glu Trp Trp Ile Gly His Ile Asp Gly Asp Pro Gly Arg
213          980          985          990

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218 <210> SEQ ID NO: 2
219 <211> LENGTH: 826
220 <212> TYPE: PRT
221 <213> ORGANISM: Mus musculus
223 <400> SEQUENCE: 2
224 Met Ile Arg Thr Glu Ile Ser Gly Ala Glu Ile Ala Glu Glu Met Glu
225 1          5          10          15
227 Lys Glu Arg Arg Phe Phe Gln Leu Gln Met Cys Glu Tyr Leu Leu Lys
228          20          25          30
230 Val Asn Glu Ile Lys Val Lys Lys Gly Val Asp Leu Leu Gln Asn Leu
231          35          40          45
233 Ile Lys Tyr Phe His Ala Gln Cys Asn Phe Phe Gln Asp Gly Leu Lys
234          50          55          60
236 Ala Val Glu Ser Leu Lys Pro Ser Ile Glu Thr Leu Ser Thr Asp Leu
237 65          70          75          80
239 His Thr Ile Lys Gln Ala Gln Asp Glu Glu Arg Arg Gln Leu Ile Gln
240          85          90          95
242 Leu Arg Asp Ile Leu Lys Ser Ala Leu Gln Val Glu Gln Lys Glu Asp
243          100          105          110
245 Ser Gln Ile Arg Gln Ser Thr Ala Tyr Ser Leu His Gln Pro Gln Gly
246          115          120          125
248 Asn Lys Glu His Gly Thr Glu Arg Asn Gly Asn Leu Tyr Lys Lys Ser
249          130          135          140
251 Asp Gly Ile Arg Lys Val Trp Gln Lys Arg Lys Cys Ser Val Lys Asn
252 145          150          155          160
254 Gly Phe Leu Thr Ile Ser His Gly Thr Ala Asn Arg Pro Pro Ala Lys
255          165          170          175
257 Leu Asn Leu Leu Thr Cys Gln Val Lys Thr Asn Pro Glu Glu Lys Lys
258          180          185          190
260 Cys Phe Asp Leu Ile Ser His Asp Arg Thr Tyr His Phe Gln Ala Glu
261          195          200          205
263 Asp Glu Gln Glu Cys Gln Ile Trp Met Ser Val Leu Gln Asn Ser Lys
264          210          215          220
266 Glu Glu Ala Leu Asn Asn Ala Phe Lys Gly Asp Asp Asn Thr Gly Glu
267 225          230          235          240
269 Asn Asn Ile Val Gln Glu Leu Thr Lys Glu Ile Ile Ser Glu Val Gln
270          245          250          255
272 Arg Met Thr Gly Asn Asp Val Cys Cys Asp Cys Gly Ala Pro Asp Pro
273          260          265          270
275 Thr Trp Leu Ser Thr Asn Leu Gly Ile Leu Thr Cys Ile Glu Cys Ser
276          275          280          285
278 Gly Ile His Arg Glu Leu Gly Val His Tyr Ser Pro Met Gln Ser Leu
279          290          295          300
281 Thr Leu Asp Val Leu Gly Thr Ser Glu Leu Leu Leu Ala Lys Asn Ile
282 305          310          315          320
284 Gly Asn Ala Gly Phe Asn Glu Ile Met Glu Cys Cys Leu Pro Ser Glu
285          325          330          335

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287 Asp Pro Val Lys Pro Asn Pro Gly Ser Asp Met Ile Ala Arg Lys Asp
288          340          345          350
290 Tyr Ile Thr Ala Lys Tyr Met Glu Arg Arg Tyr Ala Arg Lys Lys His
291          355          360          365
293 Ala Asp Thr Ala Ala Lys Leu His Ser Leu Cys Glu Ala Val Lys Thr
294          370          375          380
296 Arg Asp Ile Phe Gly Leu Leu Gln Ala Tyr Ala Asp Gly Val Asp Leu
297 385          390          395          400
299 Thr Glu Lys Ile Pro Leu Ala Asn Gly His Glu Pro Asp Glu Thr Ala
300          405          410          415
302 Leu His Leu Ala Val Arg Ser Val Asp Arg Thr Ser Leu His Ile Val
303          420          425          430
305 Asp Phe Leu Val Gln Asn Ser Gly Asn Leu Asp Lys Gln Thr Gly Lys
306          435          440          445
308 Gly Ser Thr Ala Leu His Tyr Cys Cys Leu Thr Asp Asn Ala Glu Cys
309          450          455          460
311 Leu Lys Leu Leu Leu Arg Gly Lys Ala Ser Ile Glu Ile Ala Asn Glu
312 465          470          475          480
314 Ser Gly Glu Thr Pro Leu Asp Ile Ala Lys Arg Leu Lys His Glu His
315          485          490          495
317 Cys Glu Glu Leu Leu Thr Gln Ala Leu Ser Gly Arg Phe Asn Ser His
318          500          505          510
320 Val His Val Glu Tyr Glu Trp Arg Leu Leu His Glu Asp Leu Asp Glu
321          515          520          525
323 Ser Asp Asp Asp Val Asp Glu Lys Leu Gln Pro Ser Glu Asn Arg Arg
324          530          535          540
326 Glu Asp Arg Pro Val Ser Phe Tyr Gln Leu Gly Ser Ser Gln Phe Gln
327 545          550          555          560
329 Ser Asn Ala Val Ser Leu Ala Arg Asp Thr Ala Asn Leu Thr Lys Asp
330          565          570          575
332 Lys Gln Arg Gly Phe Gly Pro Ser Ile Leu Gln Asn Glu Thr Tyr Gly
333          580          585          590
335 Ala Ile Leu Ser Gly Ser Pro Pro Ser Ser Gln Ser Ile Pro Pro Ser
336          595          600          605
338 Thr Thr Ser Ala Pro Pro Leu Pro Pro Arg Asn Val Gly Lys Asp Pro
339          610          615          620
341 Leu Thr Thr Thr Pro Pro Pro Val Ala Lys Thr Ser Gly Thr Leu
342 625          630          635          640
344 Glu Ala Met Asn Gln Pro Ser Lys Ser Ser Gln Pro Gly Thr Ser Gln
345          645          650          655
347 Ser Lys Pro Pro Pro Leu Pro Pro Gln Pro Pro Ser Arg Leu Pro Gln
348          660          665          670
350 Lys Lys Pro Ala Ser Gly Ala Asp Lys Pro Thr Pro Leu Thr Asn Lys
351          675          680          685
353 Gly Gln Pro Arg Gly Pro Glu Ala Ser Gly Pro Leu Ser Asn Ala Met
354          690          695          700
356 Ala Leu Gln Pro Pro Ala Pro Met Pro Arg Lys Ser Gln Ala Thr Lys
357 705          710          715          720
359 Ser Lys Pro Lys Arg Val Lys Ala Leu Tyr Asn Cys Val Ala Asp Asn

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,22,23